

SEQUENCE LISTING

<110> Tang, Y. Tom
 Zhou, Ping
 Goodrich, Ryle
 Liu, Chenghua
 Asundi, Vinod
 Ren, Feiyan
 Zhao, Qing A.
 Yang, Yonghong
 Wehrman, Tom
 Drmanac, Radoje T.

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 Polypeptides

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<151> 2000-02-03

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Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains. The *Agrobacterium* strains were grown in the YEA medium for 24 h at 28°C. The cell concentration of the strains was adjusted to 1.0 × 10⁸ cells/ml. The cell suspension was mixed with the plant tissue and the transformation efficiency was determined. The results are shown as the mean ± SD of three independent experiments. The asterisk indicates a significant difference (*P* < 0.05) between the two strains.

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gca gaa atg aac cgc ctg ggc atg atg gta gac tta tcc cat gtc tca      860
Ala Glu Met Asn Arg Leu Gly Met Met Val Asp Leu Ser His Val Ser
195                200                205                210

gat gct gtg gca cgg cgg gcc ctg gaa gtg tca cag gca cct gtg atc      908
Asp Ala Val Ala Arg Arg Ala Leu Glu Val Ser Gln Ala Pro Val Ile
                215                220                225

ttc tcc cac tcg gct gcc cgg ggt gtg tgc aac agt gct cgg aat gtt      956
Phe Ser His Ser Ala Ala Arg Gly Val Cys Asn Ser Ala Arg Asn Val
                230                235                240

cct gat gac atc ctg cag ctt ctg aag aag aac ggt ggc gtc gtg atg     1004
Pro Asp Asp Ile Leu Gln Leu Leu Lys Lys Asn Gly Gly Val Val Met
                245                250                255

gtg tct ttg tcc atg gga gta ata cag tgc aac cca tca gcc aat gtg     1052
Val Ser Leu Ser Met Gly Val Ile Gln Cys Asn Pro Ser Ala Asn Val
                260                265                270

tcc act gtg gca gat cac ttc gac cac atc aag gct gtc att gga tcc     1100
Ser Thr Val Ala Asp His Phe Asp His Ile Lys Ala Val Ile Gly Ser
275                280                285                290

aag ttc atc ggg att ggt gga gat tat gat ggg gcc ggc aag tac agg     1148
Lys Phe Ile Gly Ile Gly Gly Asp Tyr Asp Gly Ala Gly Lys Tyr Arg
                295                300                305

aag aaa aca aag tgc aaa gcc cct tgg agg aca agt tcc cgg atg agc     1196
Lys Lys Thr Lys Cys Lys Ala Pro Trp Arg Thr Ser Ser Arg Met Ser
                310                315                320

agc tga gcagttcctg ccactccgac ctctcacgtc tgcgtcagag acagagtctg     1252
Ser *

acttcaggcc aggaactcac tgagattccc atacactgga cagccaagtt accagccaag     1312

tggtcagtct cagagtcctc cccccacatg gccccagtc ttcagttgt ggccaccttc     1372

ccagtcctta ttctgtggct ctgatgaccc agttagtcct gccagatgtc actgtagcaa     1432

gccacagaca cccacaaaag ttccctgtgt gtgcaggcac aaatatttcc tgaaataaat     1492

gttttggaca tagaaacaga aaaaaaaaaa a                                  1523

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<210> 9
<211> 1608
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (49)..(1608)

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[illegible]

24

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agc Ser	atc Ile	aat Asn 230	aaa Lys	tcc Ser	ggg Gly	gcc Ala	tct Ser 235	tat Tyr	gag Glu	aag Lys	atc Ile 240	aaa Lys 240	gaa Glu	gtg Val	att Ile	777
ggt Gly	cat His 245	ggt Gly	tgt Cys	aaa Lys	tgg Trp	acg Thr 250	ctc Leu	agc Ser	aga Arg	ttt Phe 255	ttt Phe	tcc Ser	tac Tyr	ctt Leu	cgt Arg	825
agc Ser 260	tgg Trp	gat Asp	gtg Val	gac Asp 265	gat Asp 265	ctg Leu	ctt Leu	ttg Leu	tgg Trp	aag Lys 270	aaa Lys 270	atc Ile	cac His	cgc Arg	atg Met 275	873
gtt Val	att Ile	ctc Leu	acc Thr 280	att Ile	ctc Leu	gcc Ala	att Ile	gca Ala 285	cca Pro	tct Ser 285	gtc Val	ccc Pro	ttt Phe 290	gct Ala 290	gcc Ala	921
aat Asn	tgc Cys	ttt Phe 295	gag Glu	ctc Leu	ttt Phe	ggg Gly	ttt Phe 300	gat Asp 300	att Ile	ttg Leu	att Ile	gat Asp 305	gac Asp 305	aac Asn	ttg Leu	969
aaa Lys	cca Pro 310	tgg Trp	ctt Leu	tta Leu	gag Glu	gtc Val	aac Asn 315	tac Tyr	agc Ser	cca Pro	gcc Ala 320	ttg Leu 320	acc Thr	ttg Leu	gat Asp	1017
tgt Cys	tca Ser 325	aca Thr	gat Asp	gtg Val	ttg Leu	gtg Val 330	aag Lys	aga Arg	aaa Lys	ctt Leu 335	gtc Val 335	cat His	gat Asp	att Ile	att Ile	1065
gac Asp 340	ctg Leu	att Ile	tac Tyr	tta Leu	aat Asn 345	ggt Gly	cta Leu	aga Arg	aat Asn 350	gag Glu 350	ggg Gly	aga Arg	gaa Glu	gcc Ala	agt Ser 355	1113
aat Asn	gcc Ala	aca Thr	cat His 360	gga Gly	aat Asn	tcc Ser	aac Asn	atc Ile 365	gac Asp 365	gct Ala	gca Ala	aaa Lys	agt Ser	gac Asp 370	aga Arg	1161
ggt Gly	ggg Gly	ctt Leu	gat Asp 375	gct Ala	cct Pro	gac Asp	tgt Cys	ctt Leu 380	cct Pro	tat Tyr	gat Asp	tct Ser 385	ctt Leu 385	tcg Ser	ttc Phe	1209
aca Thr	agc Ser 390	aga Arg	atg Met	tac Tyr	aac Asn	gag Glu	gat Asp 395	gac Asp	tct Ser	gtg Val	gtg Val	gag Glu 400	aaa Lys	gct Ala	gtg Val	1257
agt Ser	gtg Val 405	cgt Arg	cct Pro	gaa Glu	gct Ala	gca Ala 410	cct Pro	gcc Ala	tcc Ser	cag Gln	ctg Leu 415	gaa Glu	gga Gly	gag Glu	atg Met	1305
agt Ser 420	ggg Gly	cag Gln	gat Asp	ttt Phe	cat His 425	ctg Leu	tca Ser	aca Thr	agg Arg	gag Glu 430	atg Met	cca Pro	caa Gln	agc Ser	aag Lys 435	1353

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ccc aag tta cgg agc agg cac acg cct cac aag aca ctc atg ccc tac      1401
Pro Lys Leu Arg Ser Arg His Thr Pro His Lys Thr Leu Met Pro Tyr
      440      445      450

gcg tcc ctc ttc cag tgc cac tcc tgc aag acc aag acc tcc ccg tgt      1449
Ala Ser Leu Phe Gln Ser His Ser Cys Lys Thr Lys Thr Ser Pro Cys
      455      460      465

gtc ctg tca gac cgt ggc aaa gct cca gat ccc caa gca ggc aac ttt      1497
Val Leu Ser Asp Arg Gly Lys Ala Pro Asp Pro Gln Ala Gly Asn Phe
      470      475      480

gtt ctt gtt ttt cct ttc aat gaa gca act ctc gga gct tcc agg aat      1545
Val Leu Val Phe Pro Phe Asn Glu Ala Thr Leu Gly Ala Ser Arg Asn
      485      490      495

gga tta aat gtc aaa aga ata atc caa gag ctc cag aaa cta atg aat      1593
Gly Leu Asn Val Lys Arg Ile Ile Gln Glu Leu Gln Lys Leu Met Asn
500      505      510      515

aag caa cat tcc taa      1608
Lys Gln His Ser *
      520

```

```

<210> 10
<211> 1891
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (362)..(1084)

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<220>
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<222> (1)...(1891)
<223> n = a,t,c or g

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gacaaagtgg ataatctcta ccacgtgaga aacttccaac attacttgca aatcagattt      180
aatgaataaa ataaagctgt agcacttggc acattcattg ggacccttac ccaaacatta      240
tcaatattgt gtacgttatc tttattatca ggtcacaaaa gatgtcataa aagaatttgc      300
agatgacggc gtcaagtacc tggaactaag gagcacaccc agaagagaaa atgctactgg      360

a      atg act aaa aag act tat gtg gaa tct ata ctt gaa ggt ata aaa      406
      Met Thr Lys Lys Thr Tyr Val Glu Ser Ile Leu Glu Gly Ile Lys

```

	1			5			10			15						
cag	tcc	aaa	caa	gaa	aac	ttg	gac	att	gat	gtt	agg	tat	ttg	ata	gca	454
Gln	Ser	Lys	Gln	Glu	Asn	Leu	Asp	Ile	Asp	Val	Arg	Tyr	Leu	Ile	Ala	
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gtt	gac	aga	aga	ggt	ggc	cct	tta	gta	gcc	aag	gag	act	gta	aaa	ctt	502
Val	Asp	Arg	Arg	Gly	Gly	Pro	Leu	Val	Ala	Lys	Glu	Thr	Val	Lys	Leu	
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gcc	gag	gag	ttc	ttc	ctt	tct	act	gag	ggt	aca	gtt	ctt	ggc	ctt	gac	550
Ala	Glu	Glu	Phe	Phe	Leu	Ser	Thr	Glu	Gly	Thr	Val	Leu	Gly	Leu	Asp	
		50					55					60				
ctc	agt	gga	gac	cct	act	gta	gga	caa	gca	aaa	gac	ttc	ttg	gaa	cct	598
Leu	Ser	Gly	Asp	Pro	Thr	Val	Gly	Gln	Ala	Lys	Asp	Phe	Leu	Glu	Pro	
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Leu	Leu	Glu	Ala	Lys	Lys	Ala	Gly	Leu	Lys	Leu	Ala	Leu	His	Leu	Ser	
	80				85					90					95	
gag	att	cca	aac	caa	aaa	aaa	gaa	aca	caa	ata	ctc	ctg	gat	ctg	ctt	694
Glu	Ile	Pro	Asn	Gln	Lys	Lys	Glu	Thr	Gln	Ile	Leu	Leu	Asp	Leu	Leu	
				100					105					110		
cct	gac	aga	atc	ggg	cat	gga	aca	ttt	ctc	aac	tcc	ggt	gag	gga	gga	742
Pro	Asp	Arg	Ile	Gly	His	Gly	Thr	Phe	Leu	Asn	Ser	Gly	Glu	Gly	Gly	
				115				120					125			
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Ser	Leu	Asp	Leu	Val	Asp	Phe	Val	Arg	Gln	His	Arg	Ile	Pro	Leu	Glu	
		130					135					140				
ctc	tgt	ttg	acc	tca	aac	gtc	aaa	agt	cag	aca	gtt	cca	tct	tat	gac	838
Leu	Cys	Leu	Thr	Ser	Asn	Val	Lys	Ser	Gln	Thr	Val	Pro	Ser	Tyr	Asp	
	145					150					155					
cag	cac	cat	ttc	gga	ttc	tgg	tac	agc	att	gcc	cat	cct	tct	gtg	atc	886
Gln	His	His	Phe	Gly	Phe	Trp	Tyr	Ser	Ile	Ala	His	Pro	Ser	Val	Ile	
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tgt	act	gat	gat	aag	ggt	gtt	ttt	gca	aca	cac	ctt	tct	caa	gag	tac	934
Cys	Thr	Asp	Asp	Lys	Gly	Val	Phe	Ala	Thr	His	Leu	Ser	Gln	Glu	Tyr	
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Gln	Leu	Ala	Ala	Glu	Thr	Phe	Asn	Leu	Thr	Gln	Ser	Gln	Val	Trp	Asp	
			195					200					205			
ctg	tct	tat	gaa	tcc	atc	aac	tac	atc	ttt	gct	tct	gac	agc	acc	aga	1030
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		210					215					220				
tct	gaa	ctg	agg	aag	aaa</											

